STR AND SNP GENETIC ANALYSES OF THE YAVAPAI NATIVE AMERICANS USING MASSIVELY PARALLEL SEQUENCING

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Forensically-relevant genetic markers were typed for 62 Yavapai Native Americans using the Illumina MiSeq FGx Forensic Genomics System. These data are invaluable to the human identity community due to the greater genetic differentiation among Native American tribes than among other subdivisions within major populations of the United States (US). Autosomal, X-chromosomal, and Y-chromosomal short tandem repeat (STR) and identity-informative (iSNPs), ancestry-informative (aSNPs), and phenotype-informative (pSNPs) single nucleotide polymorphism (SNP) allele frequencies are reported. Sequence-based allelic variants were observed in 13 autosomal, 3 X, and 3 Y STRs. Autosomal STR observed and expected heterozygosities increased by 0.081 ± 0.068 and 0.073 ± 0.063, for those autosomal STRs with sequence variation. The combined autosomal RMPs were 2.37×10^{-26} and 2.81×10^{-29} for length-based and sequence-based alleles, respectively. Twenty-two and 25 unique Y-STR haplotypes were identified among 26 males. Of the 26 haplotypes generated, 17 were assigned to haplogroup Q, three to haplogroup R1b, two each to haplogroups E1b1b and L, and one each to haplogroups R1a and I1. Multidimensional scaling plots comparing Yavapai autosomal and Y STR markers with relevant US population groups indicated the Yavapai people are closer to Hispanic and Inupiat (Native Alaskan) groups. Male and female sequence-based X-STR RMPs were 3.28×10^{-7} and 1.22×10^{-6}, respectively. The average observed and expected heterozygosities for 94 iSNPs were 0.39 ± 0.12 and 0.39 ± 0.13, respectively, and the combined iSNP RMP was 1.08×10^{-32}. The combined STR and iSNP RMPs were 2.55×10^{-58} and 3.02×10^{-61} for length-based and sequence-based STR alleles, respectively. Ancestry and phenotypic SNP information, performed using the ForenSeq™ Universal Analysis Software, predicted black hair, brown eyes, and some probability of East Asian ancestry for all but one sample that clustered between European and Admixed American ancestry on a principal components analysis.